

Abstract of the Disclosure

The invention relates to a compound that competitively inhibits binding of CSP to *S. mutans* histidine kinase. The compound is preferably a peptide or an antibody. The compound is preferably a derivative of [SEQ ID NO:2], a fragment of [SEQ ID NO:2] or a derivative of a fragment of [SEQ ID NO:2].

43153.01 1889-00401

SEQUENCE LISTING

<110> CVITKOVITCH, Dennis

<120> SIGNAL PEPTIDES NUCLEIC ACID MOLECULES AND METHODS FOR TREATMENT OF CARIES

<130> 311/0003

<140> 2 302 861

<141> 2000-04-10

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<170> PatentIn version 3.0

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Glu Ser Leu Tyr Lys Asp Ile Arg Ser Phe Arg His Asp Tyr Leu Asn
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Gln Asp Thr Arg Tyr Asn Ile Gly His Leu Ala Asn Ile Gln Asn Asp
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Ala Ile Glu Ala Ala Phe Glu Ser Leu Asn Pro Glu Ile Gln Leu Ala
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Thr Lys Gly Ser Asn Arg Gly Ile Gly Leu Ala Lys Val Asn His Ile
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180 185 190

Met Asp Lys Arg Leu Phe Gln Cys His Arg Ser Phe Ile Val Asn Pro
195 200 205

Ala Asn Ile Thr Arg Ile Asp Arg Lys Lys Arg Leu Ala Tyr Phe Arg
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Trp Gln Gln Glu Gly Met Leu Ile Leu His Gln Leu Leu Arg Glu His
35 40 45

cca gaa tta gaa gag gat gat aca aaa ttg tat atc tat ttt aag aca 192
Pro Glu Leu Glu Glu Asp Asp Thr Lys Leu Tyr Ile Tyr Phe Lys Thr
50 55 60

cgt ttt tct aat tac att aaa gat gtt ttg cgt cag caa gaa agt cag 240
Arg Phe Ser Asn Tyr Ile Lys Asp Val Leu Arg Gln Gln Glu Ser Gln
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Lys Arg Arg Phe Asn Arg Met Ser Tyr Glu Glu Val Gly Glu Ile Glu
85 90 95

cac tgt ttg tca agt ggc ggt atg caa ttg gat gaa tat att tta ttt 336
His Cys Leu Ser Ser Gly Gly Met Gln Leu Asp Glu Tyr Ile Leu Phe
100 105 110

cgt gat agt ttg ctt gca tat aaa caa ggt ctg agt act gaa aag caa 384
Arg Asp Ser Leu Leu Ala Tyr Lys Gln Gly Leu Ser Thr Glu Lys Gln
115 120 125

gag ctg ttt gag cgc ttg gta gca ggagagcact ttttggaag gcaaagtatg 438
Glu Leu Phe Glu Arg Leu Val Ala
130 135

ctgaaagatt tacgtaaaaa attaagtgat ttttaaggaaa aa 480

<210> 23

<211> 136

<212> PRT

<213> Streptococcus mutans

<400> 23

Met Glu Glu Asp Phe Glu Ile Val Phe Asn Lys Val Lys Pro Ile Val

1	5	10	15
Trp Lys Leu Ser Arg Tyr Tyr Phe Ile Lys Met Trp Thr Arg Glu Asp	20	25	30
Trp Gln Gln Glu Gly Met Leu Ile Leu His Gln Leu Leu Arg Glu His	35	40	45
Pro Glu Leu Glu Glu Asp Asp Thr Lys Leu Tyr Ile Tyr Phe Lys Thr	50	55	60
Arg Phe Ser Asn Tyr Ile Lys Asp Val Leu Arg Gln Gln Glu Ser Gln	65	70	75
Lys Arg Arg Phe Asn Arg Met Ser Tyr Glu Glu Val Gly Glu Ile Glu	85	90	95
His Cys Leu Ser Ser Gly Gly Met Gln Leu Asp Glu Tyr Ile Leu Phe	100	105	110
Arg Asp Ser Leu Leu Ala Tyr Lys Gln Gly Leu Ser Thr Glu Lys Gln	115	120	125
Glu Leu Phe Glu Arg Leu Val Ala	130	135	

<210> 24

<211> 680

<212> DNA

<213> Streptococcus mutans

<220>

<221> misc_feature

<222> (1)..(680)

<400> 24

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tttataataa ttttattata aaaggaggtc atcgtaatag atggaagaag attttgaaat 120

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tgtttttaat aaggtaagc caattgtatg gaaattaagc cgttattact ttattaaaat 180
gtggactcgt gaagattggc aacaagaggg aatgttgatt ttgcaccaat tattaaggga 240
acatccagaa ttagaagagg atgatacaaa attgtatatc tattttaaga cacgtttttc 300
taattacatt aaagatgttt tgcgtcagca agaaagtcag aaacgtcgtt ttaatagaat 360
gtcttatgaa gaagtcggtg agattgaaca ctgtttgtca agtggcggta tgcaattgga 420
tgaatatatt ttatttcgtg atagtttgct tgcataataa caaggtctga gtactgaaaa 480
gcaagagctg tttgagcgtg tggtagcagg agagcacttt ttgggaaggc aaagtatgct 540
gaaagattta cgtaaaaaat taagtgattt taaggaaaaa tagttaaaaa gggaaagaat 600
ggaacatgtg attgtacat tctttttggt tgaaaattaa gaaaagttat tataaattat 660
tggtttaaca tgccatatta 680

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<210> 25

<211> 2280

<212> DNA

<213> Streptococcus mutans

<220>

<221> CDS

<222> (1) .. (2280)

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<400> 25
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Met Lys Gln Val Ile Tyr Val Val Leu Ile Val Ile Ala Val Asn Ile
1 5 10 15

ctc tta gag att atc aaa aga gta aca aaa agg gga ggg aca gtt tcg 96
Leu Leu Glu Ile Ile Lys Arg Val Thr Lys Arg Gly Gly Thr Val Ser
20 25 30

tca tct aat cct tta cca gat ggg cag tct aag ttg ttt tgg cgc aga 144
Ser Ser Asn Pro Leu Pro Asp Gly Gln Ser Lys Leu Phe Trp Arg Arg
35 40 45

cat tat aag cta gta cct cag att gat acc aga gac tgt ggg ccg gca 192
His Tyr Lys Leu Val Pro Gln Ile Asp Thr Arg Asp Cys Gly Pro Ala
50 55 60

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gtg ctg gca tct gtt gca aag cat tac gga tct aat tac tct atc gct Val Leu Ala Ser Val Ala Lys His Tyr Gly Ser Asn Tyr Ser Ile Ala 65 70 75 80	240
tat ctg cgg gaa ctc tca aag act aac aag cag gga aca aca gct ctt Tyr Leu Arg Glu Leu Ser Lys Thr Asn Lys Gln Gly Thr Thr Ala Leu 85 90 95	288
ggc att gtt gaa gct gct aaa aag tta ggc ttt gaa aca cgc tct atc Gly Ile Val Glu Ala Ala Lys Lys Leu Gly Phe Glu Thr Arg Ser Ile 100 105 110	336
aag gcg gat atg acg ctt ttt gat tat aat gat ttg acc tat cct ttt Lys Ala Asp Met Thr Leu Phe Asp Tyr Asn Asp Leu Thr Tyr Pro Phe 115 120 125	384
atc gtc cat gtg att aaa gga aaa cgt ctg cag cat tat tat gtc gtc Ile Val His Val Ile Lys Gly Lys Arg Leu Gln His Tyr Tyr Val Val 130 135 140	432
tat ggc agc cag aat aat cag ctg att att gga gat cct gat cct tca Tyr Gly Ser Gln Asn Asn Gln Leu Ile Ile Gly Asp Pro Asp Pro Ser 145 150 155 160	480
gtt aag gtg act agg atg agt aag gaa cgc ttt caa tca gag tgg aca Val Lys Val Thr Arg Met Ser Lys Glu Arg Phe Gln Ser Glu Trp Thr 165 170 175	528
ggc ctt gca att ttc cta gct cct cag cct aac tat aag cct cat aaa Gly Leu Ala Ile Phe Leu Ala Pro Gln Pro Asn Tyr Lys Pro His Lys 180 185 190	576
ggt gaa aaa aat ggt ttg tct aat ttc ttc ccg ttg atc ttt aag cag Gly Glu Lys Asn Gly Leu Ser Asn Phe Phe Pro Leu Ile Phe Lys Gln 195 200 205	624
aaa gct ttg atg act tat att atc ata gct agc ttg att gtg acg ctc Lys Ala Leu Met Thr Tyr Ile Ile Ile Ala Ser Leu Ile Val Thr Leu 210 215 220	672
att gat att gtc gga tca tac tat ctc caa gga ata ttg gac gag tac Ile Asp Ile Val Gly Ser Tyr Tyr Leu Gln Gly Ile Leu Asp Glu Tyr 225 230 235 240	720
att cct gat cag ctg att tca act tta gga atg att acg att ggt ctg Ile Pro Asp Gln Leu Ile Ser Thr Leu Gly Met Ile Thr Ile Gly Leu 245 250 255	768
ata ata acc tat att atc cag cag gtc atg gct ttt gca aaa gaa tac Ile Ile Thr Tyr Ile Ile Gln Gln Val Met Ala Phe Ala Lys Glu Tyr 260 265 270	816
ctc ttg gcc gta ctc agt ttg cgt tta gtc att gat gtt atc ctg tct Leu Leu Ala Val Leu Ser Leu Arg Leu Val Ile Asp Val Ile Leu Ser 275 280 285	864
tat atc aaa cat att ttt acg ctt cct atg tct ttc ttt gcg aca agg	912

Tyr 300	Ile 290	Lys	His	Ile	Phe	Thr 295	Leu	Pro	Met	Ser	Phe 300	Phe	Ala	Thr	Arg	
cga Arg 305	aca Thr	gga Gly	gaa Glu	atc Ile	acg Thr 310	tct Ser	cgt Arg	ttt Phe	aca Thr	gat Asp 315	gcc Ala	aat Asn	cag Gln	att Ile	att Ile 320	960
gat Asp	gct Ala	gta Val	gcg Ala	tca Ser 325	acc Thr	atc Ile	ttt Phe	tca Ser	atc Ile 330	ttt Phe	tta Leu	gat Asp	atg Met	act Thr 335	atg Met	1008
gta Val	att Ile	ttg Leu	gtt Val	ggg Gly 340	gtt Gly	ttg Val	ttg Leu	gcg Ala	caa Gln	aac Asn	aat Asn	aac Asn	ctt Leu	ttc Phe		1056
ttt Phe	cta Leu	acc Thr 355	ttg Leu	ctc Leu	tcc Ser	att Ile	ccg Pro 360	att Ile	tat Tyr	gcc Ala	atc Ile	att Ile	att Ile	ttt Phe	gct Ala	1104
ttc Phe	ttg Leu 370	aaa Lys	ccc Pro	ttt Phe	gag Glu	aaa Lys 375	atg Met	aat Asn	cac His	gaa Glu	gtg Val	atg Met	gaa Glu	agc Ser	aat Asn	1152
gct Ala 385	gtg Val	gta Val	agt Ser	tct Ser 390	tct Ser	atc Ile	att Ile	gaa Glu	gat Asp	atc Ile 395	aat Asn	ggg Gly	atg Met	gaa Glu	acc Thr 400	1200
att Ile	aaa Lys	tca Ser	ctc Leu	aca Thr 405	agt Ser	gag Glu	tcc Ser	gct Ala	cgt Arg 410	tat Tyr	caa Gln	aac Asn	att Ile	gat Asp 415	agt Ser	1248
gaa Glu	ttt Phe	gtt Val	gat Asp 420	tat Tyr	ttg Leu	gag Glu	aaa Lys	aac Asn	ttt Phe	aag Lys	cta Leu	cac His	aag Lys	tat Tyr	agt Ser	1296
gcc Ala	att Ile	caa Gln 435	acc Thr	gca Ala	tta Leu	aaa Lys	agc Ser 440	ggt Gly	gct Ala	aag Lys	ctt Leu	atc Ile	ctc Leu	aat Asn	gtt Val	1344
gtc Val	att Ile 450	ctc Leu	tgg Trp	tat Tyr	ggc Gly	tct Ser 455	cgt Arg	cta Leu	gtt Val	atg Met	gat Asp 460	aat Asn	aaa Lys	atc Ile	tca Ser	1392
gtt Val 465	ggg Gly	cag Gln	ctt Leu	atc Ile	acc Thr 470	ttt Phe	aat Asn	gct Ala	ttg Leu	ctg Leu	tct Ser	tat Tyr	ttc Phe	tca Ser	aat Asn 480	1440
cca Pro	att Ile	gaa Glu	aat Asn	att Ile 485	atc Ile	aat Asn	ctg Leu	caa Gln	tcc Ser 490	aaa Lys	ctg Leu	cag Gln	tca Ser	gct Ala	cgc Arg 495	1488
gtt Val	gcc Ala	aat Asn	aca Thr 500	cgt Arg	ctt Leu	aat Asn	gag Glu	gtc Val 505	tat Tyr	ctt Leu	gtc Val	gaa Glu	tct Ser	gaa Glu	ttt Phe	1536
gaa Glu	aaa Lys	gac Asp	ggc Gly	gat Asp	tta Leu	tca Ser	gaa Glu	aat Asn	agc Ser	ttt Phe	tta Leu	gat Asp	ggg Gly	gat Asp	att Ile	1584

515	520	525	
tcg ttt gaa aat ctt tct tat aaa tat gga ttt ggg cga gat acc tta Ser Phe Glu Asn Leu Ser Tyr Lys Tyr Gly Phe Gly Arg Asp Thr Leu 530 535 540			1632
tca gat att aat tta tca atc aaa aaa ggc tcc aag gtc agt cta gtt Ser Asp Ile Asn Leu Ser Ile Lys Lys Gly Ser Lys Val Ser Leu Val 545 550 555 560			1680
gga gcc agt ggt tct ggt aaa aca act ttg gct aaa ctg att gtc aat Gly Ala Ser Gly Ser Gly Lys Thr Thr Leu Ala Lys Leu Ile Val Asn 565 570 575			1728
ttc tac gag cct aac aag ggg att gtt cga atc aat ggc aat gat tta Phe Tyr Glu Pro Asn Lys Gly Ile Val Arg Ile Asn Gly Asn Asp Leu 580 585 590			1776
aaa gtt att gat aag aca gct ttg cgg cgg cat att agc tat ttg ccg Lys Val Ile Asp Lys Thr Ala Leu Arg Arg His Ile Ser Tyr Leu Pro 595 600 605			1824
caa cag gcc tat gtt ttt agt ggc tct att atg gat aat ctc gtt tta Gln Gln Ala Tyr Val Phe Ser Gly Ser Ile Met Asp Asn Leu Val Leu 610 615 620			1872
gga gct aaa gaa gga acg agt cag gaa gac att att cgt gct tgt gaa Gly Ala Lys Glu Gly Thr Ser Gln Glu Asp Ile Ile Arg Ala Cys Glu 625 630 635 640			1920
att gct gaa atc cgc tcg gac att gaa caa atg cct cag ggc tat cag Ile Ala Glu Ile Arg Ser Asp Ile Glu Gln Met Pro Gln Gly Tyr Gln 645 650 655			1968
aca gag tta tca gat ggt gcc ggt att tct ggc ggt caa aaa cag cgg Thr Glu Leu Ser Asp Gly Ala Gly Ile Ser Gly Gly Gln Lys Gln Arg 660 665 670			2016
att gct tta gct agg gcc tta tta aca cag gca ccg gtt ttg att ctg Ile Ala Leu Ala Arg Ala Leu Leu Thr Gln Ala Pro Val Leu Ile Leu 675 680 685			2064
gat gaa gcc acc agc agt ctt gat att ttg aca gaa aag aaa att atc Asp Glu Ala Thr Ser Ser Leu Asp Ile Leu Thr Glu Lys Lys Ile Ile 690 695 700			2112
agc aat ctc tta cag atg acg gag aaa aca ata att ttt gtt gcc cac Ser Asn Leu Leu Gln Met Thr Glu Lys Thr Ile Ile Phe Val Ala His 705 710 715 720			2160
cgc tta agc att tca cag cgt act gac gaa gtc att gtc atg gat cag Arg Leu Ser Ile Ser Gln Arg Thr Asp Glu Val Ile Val Met Asp Gln 725 730 735			2208
gga aaa att gtt gaa caa ggc act cat aag gaa ctt tta gct aag caa Gly Lys Ile Val Glu Gln Gly Thr His Lys Glu Leu Leu Ala Lys Gln 740 745 750			2256

ggt ttc tat tat aac ctg ttt aat
 Gly Phe Tyr Tyr Asn Leu Phe Asn
 755 760

2280

<210> 26

<211> 760

<212> PRT

<213> Streptococcus mutans

<400> 26

Met Lys Gln Val Ile Tyr Val Val Leu Ile Val Ile Ala Val Asn Ile
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Leu Leu Glu Ile Ile Lys Arg Val Thr Lys Arg Gly Gly Thr Val Ser
 20 25 30

Ser Ser Asn Pro Leu Pro Asp Gly Gln Ser Lys Leu Phe Trp Arg Arg
 35 40 45

His Tyr Lys Leu Val Pro Gln Ile Asp Thr Arg Asp Cys Gly Pro Ala
 50 55 60

Val Leu Ala Ser Val Ala Lys His Tyr Gly Ser Asn Tyr Ser Ile Ala
 65 70 75 80

Tyr Leu Arg Glu Leu Ser Lys Thr Asn Lys Gln Gly Thr Thr Ala Leu
 85 90 95

Gly Ile Val Glu Ala Ala Lys Lys Leu Gly Phe Glu Thr Arg Ser Ile
 100 105 110

Lys Ala Asp Met Thr Leu Phe Asp Tyr Asn Asp Leu Thr Tyr Pro Phe
 115 120 125

Ile Val His Val Ile Lys Gly Lys Arg Leu Gln His Tyr Tyr Val Val
 130 135 140

Tyr Gly Ser Gln Asn Asn Gln Leu Ile Ile Gly Asp Pro Asp Pro Ser
 145 150 155 160

Val Lys Val Thr Arg Met Ser Lys Glu Arg Phe Gln Ser Glu Trp Thr
165 170 175

Gly Leu Ala Ile Phe Leu Ala Pro Gln Pro Asn Tyr Lys Pro His Lys
180 185 190

Gly Glu Lys Asn Gly Leu Ser Asn Phe Phe Pro Leu Ile Phe Lys Gln
195 200 205

Lys Ala Leu Met Thr Tyr Ile Ile Ile Ala Ser Leu Ile Val Thr Leu
210 215 220

Ile Asp Ile Val Gly Ser Tyr Tyr Leu Gln Gly Ile Leu Asp Glu Tyr
225 230 235 240

Ile Pro Asp Gln Leu Ile Ser Thr Leu Gly Met Ile Thr Ile Gly Leu
245 250 255

Ile Ile Thr Tyr Ile Ile Gln Gln Val Met Ala Phe Ala Lys Glu Tyr
260 265 270

Leu Leu Ala Val Leu Ser Leu Arg Leu Val Ile Asp Val Ile Leu Ser
275 280 285

Tyr Ile Lys His Ile Phe Thr Leu Pro Met Ser Phe Phe Ala Thr Arg
290 295 300

Arg Thr Gly Glu Ile Thr Ser Arg Phe Thr Asp Ala Asn Gln Ile Ile
305 310 315 320

Asp Ala Val Ala Ser Thr Ile Phe Ser Ile Phe Leu Asp Met Thr Met
325 330 335

Val Ile Leu Val Gly Gly Val Leu Leu Ala Gln Asn Asn Asn Leu Phe
340 345 350

Phe Leu Thr Leu Leu Ser Ile Pro Ile Tyr Ala Ile Ile Ile Phe Ala
355 360 365

Phe Leu Lys Pro Phe Glu Lys Met Asn His Glu Val Met Glu Ser Asn
370 375 380

Ala Val Val Ser Ser Ser Ile Ile Glu Asp Ile Asn Gly Met Glu Thr
385 390 395 400

Ile Lys Ser Leu Thr Ser Glu Ser Ala Arg Tyr Gln Asn Ile Asp Ser
405 410 415

Glu Phe Val Asp Tyr Leu Glu Lys Asn Phe Lys Leu His Lys Tyr Ser
420 425 430

Ala Ile Gln Thr Ala Leu Lys Ser Gly Ala Lys Leu Ile Leu Asn Val
435 440 445

Val Ile Leu Trp Tyr Gly Ser Arg Leu Val Met Asp Asn Lys Ile Ser
450 455 460

Val Gly Gln Leu Ile Thr Phe Asn Ala Leu Leu Ser Tyr Phe Ser Asn
465 470 475 480

Pro Ile Glu Asn Ile Ile Asn Leu Gln Ser Lys Leu Gln Ser Ala Arg
485 490 495

Val Ala Asn Thr Arg Leu Asn Glu Val Tyr Leu Val Glu Ser Glu Phe
500 505 510

Glu Lys Asp Gly Asp Leu Ser Glu Asn Ser Phe Leu Asp Gly Asp Ile
515 520 525

Ser Phe Glu Asn Leu Ser Tyr Lys Tyr Gly Phe Gly Arg Asp Thr Leu
530 535 540

Ser Asp Ile Asn Leu Ser Ile Lys Lys Gly Ser Lys Val Ser Leu Val
545 550 555 560

Gly Ala Ser Gly Ser Gly Lys Thr Thr Leu Ala Lys Leu Ile Val Asn
565 570 575

Phe Tyr Glu Pro Asn Lys Gly Ile Val Arg Ile Asn Gly Asn Asp Leu
580 585 590

Lys Val Ile Asp Lys Thr Ala Leu Arg Arg His Ile Ser Tyr Leu Pro
595 600 605

Gln Gln Ala Tyr Val Phe Ser Gly Ser Ile Met Asp Asn Leu Val Leu

610	615	620
Gly Ala Lys Glu Gly Thr Ser Gln Glu Asp Ile Ile Arg Ala Cys Glu		
625	630	635 640
Ile Ala Glu Ile Arg Ser Asp Ile Glu Gln Met Pro Gln Gly Tyr Gln		
	645	650 655
Thr Glu Leu Ser Asp Gly Ala Gly Ile Ser Gly Gly Gln Lys Gln Arg		
	660	665 670
Ile Ala Leu Ala Arg Ala Leu Leu Thr Gln Ala Pro Val Leu Ile Leu		
	675	680 685
Asp Glu Ala Thr Ser Ser Leu Asp Ile Leu Thr Glu Lys Lys Ile Ile		
	690	695 700
Ser Asn Leu Leu Gln Met Thr Glu Lys Thr Ile Ile Phe Val Ala His		
705	710	715 720
Arg Leu Ser Ile Ser Gln Arg Thr Asp Glu Val Ile Val Met Asp Gln		
	725	730 735
Gly Lys Ile Val Glu Gln Gly Thr His Lys Glu Leu Leu Ala Lys Gln		
	740	745 750
Gly Phe Tyr Tyr Asn Leu Phe Asn		
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<210> 27

<211> 900

<212> DNA

<213> Streptococcus mutans

<220>

<221> CDS

<222> (1) .. (900)

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 100 105 110

Glu Glu Lys Glu Lys Lys Lys His Gln Lys Ser Lys Lys Lys Lys Lys
 115 120 125

Ser Lys Ser Lys Lys Ala Ser Lys Asp Lys Lys Lys Lys Ser Lys Asp
 130 135 140

Lys Glu Ser Ser Ser Asp Asp Glu Asn Glu Thr Lys Lys Val Ser Ile
 145 150 155 160

Phe Ala Ser Glu Asp Gly Ile Ile His Thr Asn Pro Lys Tyr Asp Gly
 165 170 175

Ala Asn Ile Ile Pro Lys Gln Thr Glu Ile Ala Gln Ile Tyr Pro Asp
 180 185 190

Ile Gln Lys Thr Arg Lys Val Leu Ile Thr Tyr Tyr Ala Ser Ser Asp
 195 200 205

Asp Val Val Ser Met Lys Lys Gly Gln Thr Ala Arg Leu Ser Leu Glu
 210 215 220

Lys Lys Gly Asn Asp Lys Val Val Ile Glu Gly Lys Ile Asn Asn Val
 225 230 235 240

Ala Ser Ser Ala Thr Thr Thr Lys Lys Gly Asn Leu Phe Lys Val Thr
 245 250 255

Ala Lys Val Lys Val Ser Lys Lys Asn Ser Lys Leu Ile Lys Tyr Gly
 260 265 270

Met Thr Gly Lys Thr Val Thr Val Ile Asp Lys Lys Thr Tyr Phe Asp
 275 280 285

Tyr Phe Lys Asp Lys Leu Leu His Lys Met Asp Asn
 290 295 300